

SEQUENCE LISTING

<110> SODE, Koji

<120> Glucose dehydrogenase beta-subunit and DNA encoding the same

<130> TOYA126.002APC

<141> 2003-04-25

<150> JP 2002-125353

<151> 2002-04-26

<160> 19

<170> PatentIn Ver. 2.0

<210> 1

<211> 2467

<212> DNA

<213> Burkholderia cepacia

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<221> CDS

<222> (258) .. (761)

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Gly Ala Leu Ala Leu Thr Ala Ala Gly Leu Thr Gly Ser Leu Thr Leu
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Thr Leu Ser Glu Ser Leu Thr Gly Lys Lys Gly Leu Ser Arg Val Ile
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Lys Leu Ile Glu Asn Ala Val Val Tyr Lys Leu Glu Thr Gly Pro Asp			
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Thr Gly Val Ser Phe Tyr Ala Ser Glu Lys Leu Trp Pro Gly Arg Gly			
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<210> 2

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<212> PRT

<213> Burkholderia cepacia

<400> 2

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 Asn Pro Gly Thr Ala Pro Leu Asp Thr Phe Met Thr Leu Ser Glu Ser
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 85 90 95
 Leu Ala Gly Ala Leu Ala Ser Gly Ser Leu Thr Pro Glu Gln Glu Ser
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<212> PRT

<213> Burkholderia cepacia

<400> 3

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 <213> Burkholderia cepacia

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 <213> Burkholderia cepacia

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 <212> PRT
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 <223> Xaa=unknown

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 20 25

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 <212> DNA
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<220>
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 ggaagtctga cc gtg cgg aaa tct act ctc acc ttc ctc ctc gcc ggc tgc 711
 Val Arg Lys Ser Thr Leu Thr Phe Leu Leu Ala Gly Cys
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 cat gtc aag cgc ggc gaa tac ctc gcc gtc gcg ggc gac tgc atg gca 807
 His Val Lys Arg Gly Glu Tyr Leu Ala Val Ala Gly Asp Cys Met Ala
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Cys	His	Thr	Ala	Lys	Gly	Gly	Lys	Pro	Phe	Ala	Gly	Gly	Leu	Gly	Met	
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ccg	gtg	ccg	atg	ctc	ggc	aag	atc	tat	acg	agc	aac	atc	aca	ccg	gat	903
Pro	Val	Pro	Met	Leu	Gly	Lys	Ile	Tyr	Thr	Ser	Asn	Ile	Thr	Pro	Asp	
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ccc	gat	acc	ggc	atc	ggc	aac	tgg	acg	ttc	gag	gac	ttc	gag	cgc	gcg	951
Pro	Asp	Thr	Gly	Ile	Gly	Asn	Trp	Thr	Phe	Glu	Asp	Phe	Glu	Arg	Ala	
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Val	Arg	His	Gly	Val	Ser	Lys	Asn	Gly	Asp	Asn	Leu	Tyr	Pro	Ala	Met	
	95					100					105					
ccg	tac	gtg	tcg	tac	gcg	aag	atc	aac	gac	gac	gac	gtg	caa	gcg	ctg	1047
Pro	Tyr	Val	Ser	Tyr	Ala	Lys	Ile	Asn	Asp	Asp	Asp	Val	Gln	Ala	Leu	
110					115					120					125	
tac	gcg	tac	ttc	atg	cac	ggc	gtc	gaa	ccg	gtc	aag	cag	gcg	ccg	ccg	1095
Tyr	Ala	Tyr	Phe	Met	His	Gly	Val	Glu	Pro	Val	Lys	Gln	Ala	Pro	Pro	
				130					135					140		
aag	aac	gag	atc	ccc	gcg	ctg	ctg	agc	atg	cgc	tgg	ccg	ctg	aag	atc	1143
Lys	Asn	Glu	Ile	Pro	Ala	Leu	Leu	Ser	Met	Arg	Trp	Pro	Leu	Lys	Ile	
			145					150					155			
tgg	aac	tgg	ctg	ttc	ctg	aag	gac	ggc	gtg	tac	cag	ccg	aag	ccc	gag	1191
Trp	Asn	Trp	Leu	Phe	Leu	Lys	Asp	Gly	Val	Tyr	Gln	Pro	Lys	Pro	Glu	
		160					165					170				
cag	agc	gcc	gag	tgg	aac	cgc	ggc	gcc	tat	ctc	gtg	cag	ggc	ctc	gcg	1239
Gln	Ser	Ala	Glu	Trp	Asn	Arg	Gly	Ala	Tyr	Leu	Val	Gln	Gly	Leu	Ala	
		175				180					185					
cac	tgc	agc	acg	tgc	cac	acg	ccg	cgc	ggc	atc	gcg	atg	cag	gag	aag	1287
His	Cys	Ser	Thr	Cys	His	Thr	Pro	Arg	Gly	Ile	Ala	Met	Gln	Glu	Lys	
190						195				200					205	
tcg	ctc	gac	gaa	acg	ggc	ggc	agc	ttc	ctg	tcg	ggc	tcg	gtg	ctc	gcg	1335
Ser	Leu	Asp	Glu	Thr	Gly	Gly	Ser	Phe	Leu	Ser	Gly	Ser	Val	Leu	Ala	
				210					215					220		
ggc	tgg	gac	ggc	tac	aac	atc	acg	tcc	gac	ccg	aac	gcg	ggg	atc	ggc	1383
Gly	Trp	Asp	Gly	Tyr	Asn	Ile	Thr	Ser	Asp	Pro	Asn	Ala	Gly	Ile	Gly	
			225					230					235			
ggc	tgg	acg	cag	cag	cag	ctc	gtc	cag	tac	ctg	cgc	acc	ggc	agc	gtg	1431
Gly	Trp	Thr	Gln	Gln	Gln	Leu	Val	Gln	Tyr	Leu	Arg	Thr	Gly	Ser	Val	
			240				245					250				
ccg	ggc	ctc	gcg	cag	gcg	gcc	ggc	ccg	atg	gcc	gag	gcg	atc	gag	cac	1479
Pro	Gly	Leu	Ala	Gln	Ala	Ala	Gly	Pro	Met	Ala	Glu	Ala	Ile	Glu	His	
			255			260					265					
agc	ttc	tcg	aag	atg	acc	gaa	gcc	gac	atc	ggc	ggc	ccg	atg	gcc	gag	1527
Ser	Phe	Ser	Lys	Met	Thr	Glu	Ala	Asp	Ile	Gly	Gly	Pro	Met	Ala	Glu	
270					275					280					285	
gcg	atc	gag	cac	agc	ttc	tcg	aag	atg	acc	gaa	gcc	gac	atc	ggc	cgc	1575
Ala	Ile	Glu	His	Ser	Phe	Ser	Lys	Met	Thr	Glu	Ala	Asp	Ile	Gly	Arg	
				290					295					300		
tcg	tcg	tgg	ggc	aag	ccg	gcc	gag	gat	ggc	ctg	aag	ctg	cgc	ggc	gtc	1623
Ser	Ser	Trp	Gly	Lys	Pro	Ala	Glu	Asp	Gly	Leu	Lys	Leu	Arg	Gly	Val	
			305					310					315			
gcg	ctc	gcg	tcg	tcg	ggc	atc	gat	ccg	gca	ccg	ctg	tat	ctc	ggc	aac	1671
Ala	Leu	Ala	Ser	Ser	Gly	Ile	Asp	Pro	Ala	Pro	Leu	Tyr	Leu	Gly	Asn	
			320				325					330				
tgc	gcg	acc	tgc	cac	cag	atg	cag	ggc	aag	ggc	acg	ccg	gac	ggt	tac	1719
Cys	Ala	Thr	Cys	His	Gln	Met	Gln	Gly	Lys	Gly	Thr	Pro	Asp	Gly	Tyr	
		335				340					345					

tac ccg ccg ttg ttc cac aac tcg acg gtc ggc gcg tcg aat ccg acc	1767
Tyr Pro Pro Leu Phe His Asn Ser Thr Val Gly Ala Ser Asn Pro Thr	
350 355 360 365	
aac ctc gtg cag gtg atc ctg aac ggc gtg cag cgc aag gcc ggc agc	1815
Asn Leu Val Gln Val Ile Leu Asn Gly Val Gln Arg Lys Ala Gly Ser	
370 375 380	
gag gac gtc ggg atg ccc gcg ttc cgc cac gag ctg tcg gat gcg cag	1863
Glu Asp Val Gly Met Pro Ala Phe Arg His Glu Leu Ser Asp Ala Gln	
385 390 395	
atc gcc gcg ctg acg aac tac ctg acg ggc cag ttc ggc aat ccg gcc	1911
Ile Ala Ala Leu Thr Asn Tyr Leu Thr Gly Gln Phe Gly Asn Pro Ala	
400 405 410	
gcg aag gtg acc gag cag gac gtc gcg aag ctg cgc tga aacgcggcac	1960
Ala Lys Val Thr Glu Gln Asp Val Ala Lys Leu Arg	
415 420 425	
gcggcgaggc agggcaacaa tagaaaagag gaggagcaca gcacatcggg cgggccccga	2020
tgccggttgt tgcagagcgg gacgggcggc gcaggcggtc gcccgtcctg gttcacaggc	2080
aatccggtgc gcgcacgccg cgcctcgttt tcgttgatcg agaccatgac accgaaccaa	2140
ccgtttctcg cgtcccagcg cgatgtgctg ctgctgctgt cccgaatcct gctcgtgatc	2200
ctgttcgtga tgttcggctg gaagaagatt atcgacttct ccggtacgat cgcgttcgat	2260
ggcagcgagg gcgcgccggc gccgatcatc tcggcggcga tctccgtcgt gatggagctc	2320
atcgtcggga ttgcgacccg cgtcggtttc cagacgcggc cgctcgcgct gttgcttgcg	2380
ctgtacacga tcggtaccgg catcatcggc	2410

<210> 12

<211> 425

<212> PRT

<213> Burkholderia cepacia

<400> 12

Val Arg Lys Ser Thr Leu Thr Phe Leu Leu Ala Gly Cys Leu Ala Leu	
1 5 10 15	
Pro Gly Leu Ala Arg Ala Ala Asp Ser Ala Asp Pro Ala His Val Lys	
20 25 30	
Arg Gly Glu Tyr Leu Ala Val Ala Gly Asp Cys Met Ala Cys His Thr	
35 40 45	
Ala Lys Gly Gly Lys Pro Phe Ala Gly Gly Leu Gly Met Pro Val Pro	
50 55 60	
Met Leu Gly Lys Ile Tyr Thr Ser Asn Ile Thr Pro Asp Pro Asp Thr	
65 70 75 80	
Gly Ile Gly Asn Trp Thr Phe Glu Asp Phe Glu Arg Ala Val Arg His	
85 90 95	
Gly Val Ser Lys Asn Gly Asp Asn Leu Tyr Pro Ala Met Pro Tyr Val	
100 105 110	
Ser Tyr Ala Lys Ile Asn Asp Asp Asp Val Gln Ala Leu Tyr Ala Tyr	
115 120 125	
Phe Met His Gly Val Glu Pro Val Lys Gln Ala Pro Lys Asn Glu	
130 135 140	
Ile Pro Ala Leu Leu Ser Met Arg Trp Pro Leu Lys Ile Trp Asn Trp	
145 150 155 160	
Leu Phe Leu Lys Asp Gly Val Tyr Gln Pro Lys Pro Glu Gln Ser Ala	
165 170 175	
Glu Trp Asn Arg Gly Ala Tyr Leu Val Gln Gly Leu Ala His Cys Ser	
180 185 190	
Thr Cys His Thr Pro Arg Gly Ile Ala Met Gln Glu Lys Ser Leu Asp	
195 200 205	
Glu Thr Gly Gly Ser Phe Leu Ser Gly Ser Val Leu Ala Gly Trp Asp	

210		215		220
Gly Tyr Asn Ile Thr Ser Asp Pro Asn Ala Gly Ile Gly Gly Trp Thr				
225		230		240
Gln Gln Gln Leu Val Gln Tyr Leu Arg Thr Gly Ser Val Pro Gly Leu				
	245		250	255
Ala Gln Ala Ala Gly Pro Met Ala Glu Ala Ile Glu His Ser Phe Ser				
	260		265	270
Lys Met Thr Glu Ala Asp Ile Gly Gly Pro Met Ala Glu Ala Ile Glu				
	275		280	285
His Ser Phe Ser Lys Met Thr Glu Ala Asp Ile Gly Arg Ser Ser Trp				
	290		295	300
Gly Lys Pro Ala Glu Asp Gly Leu Lys Leu Arg Gly Val Ala Leu Ala				
305		310		320
Ser Ser Gly Ile Asp Pro Ala Pro Leu Tyr Leu Gly Asn Cys Ala Thr				
	325		330	335
Cys His Gln Met Gln Gly Lys Gly Thr Pro Asp Gly Tyr Tyr Pro Pro				
	340		345	350
Leu Phe His Asn Ser Thr Val Gly Ala Ser Asn Pro Thr Asn Leu Val				
	355		360	365
Gln Val Ile Leu Asn Gly Val Gln Arg Lys Ala Gly Ser Glu Asp Val				
	370		375	380
Gly Met Pro Ala Phe Arg His Glu Leu Ser Asp Ala Gln Ile Ala Ala				
385		390		400
Leu Thr Asn Tyr Leu Thr Gly Gln Phe Gly Asn Pro Ala Ala Lys Val				
	405		410	415
Thr Glu Gln Asp Val Ala Lys Leu Arg				
	420		425	

<210> 13
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 13
 tgcaccgtgc ggaaatctac tctcact

27

<210> 14
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 14
 acttccttct tcagcgtgtc cgacatc

27

□|<210> 15
 <211> 1441
 <212> DNA
 <213> Burkholderia cepacia

<220>
 <221> CDS

<222> (121)..(1398)

<400> 15

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gctgacgacg gccgcgctcg cgctgcggat gtcggacacg ctgaagaagg aagtctgacc 120
gtg cgg aaa tct act ctc act ttc ctc atc gcc ggc tgc ctc gcg ttg 168
Val Arg Lys Ser Thr Leu Thr Phe Leu Ile Ala Gly Cys Leu Ala Leu
  1           5           10           15
ccg ggc ttc gcg cgc gcg gcc gat gcg gcc gat ccg gcg ctg gtc aag 216
Pro Gly Phe Ala Arg Ala Ala Asp Ala Ala Asp Pro Ala Leu Val Lys
      20           25           30
cgc ggc gaa tac ctc gcg acc gcc atg ccg gta ccg atg ctc ggc aag 264
Arg Gly Glu Tyr Leu Ala Thr Ala Met Pro Val Pro Met Leu Gly Lys
      35           40           45
atc tac acg agc aac atc acg ccc gat ccc gat acg ggc gac tgc atg 312
Ile Tyr Thr Ser Asn Ile Thr Pro Asp Pro Asp Thr Gly Asp Cys Met
      50           55           60
gcc tgc cac acc gtg aag ggc ggc aag ccg tac gcg ggc ggc ctt ggc 360
Ala Cys His Thr Val Lys Gly Gly Lys Pro Tyr Ala Gly Gly Leu Gly
      65           70           75           80
ggc atc ggc aaa tgg acg ttc gag gac ttc gag cgc gcg gtg cgg cac 408
Gly Ile Gly Lys Trp Thr Phe Glu Asp Phe Glu Arg Ala Val Arg His
      85           90           95
ggc gtg tcg aag aac ggc gac aac ctg tat ccg gcg atg ccg tac gtg 456
Gly Val Ser Lys Asn Gly Asp Asn Leu Tyr Pro Ala Met Pro Tyr Val
      100          105          110
tcg tac gcg aag atc aag gac gac gac gta cgc gcg ctg tac gcc tac 504
Ser Tyr Ala Lys Ile Lys Asp Asp Asp Val Arg Ala Leu Tyr Ala Tyr
      115          120          125
ttc atg cac ggc gtc gag ccg gtc aag cag gcg ccg ccg aag aac gag 552
Phe Met His Gly Val Glu Pro Val Lys Gln Ala Pro Pro Lys Asn Glu
      130          135          140
atc cca gcg ctg cta agc atg cgc tgg ccg ctg aag atc tgg aac tgg 600
Ile Pro Ala Leu Leu Ser Met Arg Trp Pro Leu Lys Ile Trp Asn Trp
      145          150          155          160
ctg ttc ctg aag gac ggc ccg tac cag ccg aag ccg tcg cag agc gcc 648
Leu Phe Leu Lys Asp Gly Pro Tyr Gln Pro Lys Pro Ser Gln Ser Ala
      165          170          175
gaa tgg aat cgc ggc gcg tat ctg gtg cag ggt ctc gcg cac tgc agc 696
Glu Trp Asn Arg Gly Ala Tyr Leu Val Gln Gly Leu Ala His Cys Ser
      180          185          190
acg tgc cac acg ccg cgc ggc atc gcg atg cag gag aag tcg ctc gac 744
Thr Cys His Thr Pro Arg Gly Ile Ala Met Gln Glu Lys Ser Leu Asp
      195          200          205
gaa acc ggc ggc agc ttc ctc gcg ggc tcg gtg ctc gcc ggc tgg gac 792
Glu Thr Gly Gly Ser Phe Leu Ala Gly Ser Val Leu Ala Gly Trp Asp
      210          215          220
ggc tac aac atc acg tcg gac ccg aat gcg ggc atc ggc agc tgg acg 840
Gly Tyr Asn Ile Thr Ser Asp Pro Asn Ala Gly Ile Gly Ser Trp Thr
      225          230          235          240
cag cag cag ctc gtg cag tat ttg cgc acc ggc agc gtg ccg ggc gtc 888
Gln Gln Gln Leu Val Gln Tyr Leu Arg Thr Gly Ser Val Pro Gly Val
      245          250          255
gcg cag gcg gcc ggg ccg atg gcc gag gcg gtc gag cac agc ttc tcg 936
Ala Gln Ala Ala Gly Pro Met Ala Glu Ala Val Glu His Ser Phe Ser
      260          265          270
aag atg acc gaa gcg gac atc ggt gcg atc gcc acg tac gtc cgc acg 984
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Lys	Met	Thr	Glu	Ala	Asp	Ile	Gly	Ala	Ile	Ala	Thr	Tyr	Val	Arg	Thr		
		275					280					285					
gtg	ccg	gcc	gtt	gcc	gac	agc	aac	gcg	aag	cag	ccg	cgg	tcg	tcg	tgg	1032	
Val	Pro	Ala	Val	Ala	Asp	Ser	Asn	Ala	Lys	Gln	Pro	Arg	Ser	Ser	Trp		
	290					295				300							
ggc	aag	ccg	gcc	gag	gac	ggg	ctg	aag	ctg	cgc	ggt	gtc	gcg	ctc	gcg	1080	
Gly	Lys	Pro	Ala	Glu	Asp	Gly	Leu	Lys	Leu	Arg	Gly	Val	Ala	Leu	Ala		
305					310					315					320		
tcg	tcg	ggc	atc	gat	ccg	gcg	cgg	ctg	tat	ctc	ggc	aac	tgc	gcg	acg	1128	
Ser	Ser	Gly	Ile	Asp	Pro	Ala	Arg	Leu	Tyr	Leu	Gly	Asn	Cys	Ala	Thr		
				325					330					335			
tgc	cac	cag	atg	cag	ggc	aag	ggc	acg	ccg	gac	ggc	tat	tac	ccg	tcg	1176	
Cys	His	Gln	Met	Gln	Gly	Lys	Gly	Thr	Pro	Asp	Gly	Tyr	Tyr	Pro	Ser		
			340					345					350				
ctg	ttc	cac	aac	tcc	acc	gtc	ggc	gcg	tcg	aat	ccg	tcg	aac	ctc	gtg	1224	
Leu	Phe	His	Asn	Ser	Thr	Val	Gly	Ala	Ser	Asn	Pro	Ser	Asn	Leu	Val		
		355					360					365					
cag	gtg	atc	ctg	aac	ggc	gtg	cag	cgc	aag	atc	ggc	agc	gag	gat	atc	1272	
Gln	Val	Ile	Leu	Asn	Gly	Val	Gln	Arg	Lys	Ile	Gly	Ser	Glu	Asp	Ile		
	370					375					380						
ggg	atg	ccc	gct	ttc	cgc	tac	gat	ctg	aac	gac	gcg	cag	atc	gcc	gcg	1320	
Gly	Met	Pro	Ala	Phe	Arg	Tyr	Asp	Leu	Asn	Asp	Ala	Gln	Ile	Ala	Ala		
385					390					395					400		
ctg	acg	aac	tac	gtg	acc	gcg	cag	ttc	ggc	aat	ccg	gcg	gcg	aag	gtg	1368	
Leu	Thr	Asn	Tyr	Val	Thr	Ala	Gln	Phe	Gly	Asn	Pro	Ala	Ala	Lys	Val		
				405					410					415			
acg	gag	cag	gac	gtc	gcg	aag	ctg	cgc	tga	catagtcggg	cgcgccgaca					1418	
Thr	Glu	Gln	Asp	Val	Ala	Lys	Leu	Arg									
			420				425										
cggcgcgaacc	gataggacag	gag														1441	

<210> 16

<211> 425

<212> PRT

<213> Burkholderia cepacia

<400> 16

Val	Arg	Lys	Ser	Thr	Leu	Thr	Phe	Leu	Ile	Ala	Gly	Cys	Leu	Ala	Leu		
1				5					10					15			
Pro	Gly	Phe	Ala	Arg	Ala	Ala	Asp	Ala	Ala	Asp	Pro	Ala	Leu	Val	Lys		
			20				25						30				
Arg	Gly	Glu	Tyr	Leu	Ala	Thr	Ala	Met	Pro	Val	Pro	Met	Leu	Gly	Lys		
		35					40					45					
Ile	Tyr	Thr	Ser	Asn	Ile	Thr	Pro	Asp	Pro	Asp	Thr	Gly	Asp	Cys	Met		
	50					55					60						
Ala	Cys	His	Thr	Val	Lys	Gly	Gly	Lys	Pro	Tyr	Ala	Gly	Gly	Leu	Gly		
65					70				75					80			
Gly	Ile	Gly	Lys	Trp	Thr	Phe	Glu	Asp	Phe	Glu	Arg	Ala	Val	Arg	His		
			85						90					95			
Gly	Val	Ser	Lys	Asn	Gly	Asp	Asn	Leu	Tyr	Pro	Ala	Met	Pro	Tyr	Val		
			100					105					110				
Ser	Tyr	Ala	Lys	Ile	Lys	Asp	Asp	Val	Arg	Ala	Leu	Tyr	Ala	Tyr			
		115					120					125					
Phe	Met	His	Gly	Val	Glu	Pro	Val	Lys	Gln	Ala	Pro	Pro	Lys	Asn	Glu		
	130					135				140							
Ile	Pro	Ala	Leu	Leu	Ser	Met	Arg	Trp	Pro	Leu	Lys	Ile	Trp	Asn	Trp		
145					150					155					160		

Leu	Phe	Leu	Lys	Asp	Gly	Pro	Tyr	Gln	Pro	Lys	Pro	Ser	Gln	Ser	Ala	
				165					170						175	
Glu	Trp	Asn	Arg	Gly	Ala	Tyr	Leu	Val	Gln	Gly	Leu	Ala	His	Cys	Ser	
			180					185						190		
Thr	Cys	His	Thr	Pro	Arg	Gly	Ile	Ala	Met	Gln	Glu	Lys	Ser	Leu	Asp	
		195					200					205				
Glu	Thr	Gly	Gly	Ser	Phe	Leu	Ala	Gly	Ser	Val	Leu	Ala	Gly	Trp	Asp	
	210					215					220					
Gly	Tyr	Asn	Ile	Thr	Ser	Asp	Pro	Asn	Ala	Gly	Ile	Gly	Ser	Trp	Thr	
225					230				235						240	
Gln	Gln	Gln	Leu	Val	Gln	Tyr	Leu	Arg	Thr	Gly	Ser	Val	Pro	Gly	Val	
				245					250					255		
Ala	Gln	Ala	Ala	Gly	Pro	Met	Ala	Glu	Ala	Val	Glu	His	Ser	Phe	Ser	
			260					265					270			
Lys	Met	Thr	Glu	Ala	Asp	Ile	Gly	Ala	Ile	Ala	Thr	Tyr	Val	Arg	Thr	
		275					280					285				
Val	Pro	Ala	Val	Ala	Asp	Ser	Asn	Ala	Lys	Gln	Pro	Arg	Ser	Ser	Trp	
	290					295					300					
Gly	Lys	Pro	Ala	Glu	Asp	Gly	Leu	Lys	Leu	Arg	Gly	Val	Ala	Leu	Ala	
305					310				315					320		
Ser	Ser	Gly	Ile	Asp	Pro	Ala	Arg	Leu	Tyr	Leu	Gly	Asn	Cys	Ala	Thr	
				325				330						335		
Cys	His	Gln	Met	Gln	Gly	Lys	Gly	Thr	Pro	Asp	Gly	Tyr	Tyr	Pro	Ser	
			340					345					350			
Leu	Phe	His	Asn	Ser	Thr	Val	Gly	Ala	Ser	Asn	Pro	Ser	Asn	Leu	Val	
		355					360					365				
Gln	Val	Ile	Leu	Asn	Gly	Val	Gln	Arg	Lys	Ile	Gly	Ser	Glu	Asp	Ile	
	370					375					380					
Gly	Met	Pro	Ala	Phe	Arg	Tyr	Asp	Leu	Asn	Asp	Ala	Gln	Ile	Ala	Ala	
385					390				395					400		
Leu	Thr	Asn	Tyr	Val	Thr	Ala	Gln	Phe	Gly	Asn	Pro	Ala	Ala	Lys	Val	
				405				410						415		
Thr	Glu	Gln	Asp	Val	Ala	Lys	Leu	Arg								
			420				425									

<210> 17

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: heme binding motif

<220>

<221> UNSURE

<222> (2,3)

<223> Xaa=unknown

<400> 17

Cys Xaa Xaa Cys His

1

5

<210> 18

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 18

catgccatgg cacacaacga caacact

27

<210> 19

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 19

cccaagcttg ggtcagactt ccttcttcag c

31